

**IN THE SPECIFICATION:**

Please replace the paragraph beginning at page 26, line 27, with the following rewritten paragraph:

**Example 3**

**QTL Analysis of Body Weight**

RIX hybrids, generated as described in Example 2, and RI parents were used to analyze body weight, which is a morphometric characteristic controlled by quantitative trait loci. The genotypes of the CXB RI parents are described by Williams *et al.* (2001) *Genome Biology* 2:0046.1-0046.18, and the genotypes of the RIX hybrids (generated as described in Example 2) were inferred from the parental genotypes. Interval mapping and composite interval mapping of loci linked to body weight were analyzed using the Map Manager QTX program (publicly available at <http://mapmgr.roswellpark.org/mmQTX.html> on the World Wide Web from [Mapmanager.org](http://Mapmanager.org)). See Manly *et al.* (2001) *Mamm Genome* 12:930-932.

Please replace the paragraph beginning at page 30, line 16, with the following rewritten paragraph:

Once a genomic interval is narrowed to less than about 0.3 cM, a list of genes positioned with the interval can be obtained from genome sequencing sources[[.]] (e.g., the Human Genome Project, <http://www.ncbi.nlm.nih.gov/HGP/> available at the website of the National Center for Biotechnology Information (NCBI)). Candidate genes are then individually tested for a role in contributing to the relevant phenotype.